Amendments to the Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims

1. (Canceled)

2. (Currently amended) A method according to any one of claims [[1]] 13, 14, 28, 29, 30, 31, 32, 33, or 34, further comprising stimulating said cells to produce germline mRNA.

3. (Currently amended) A method according to any one of claims [[1]] 13, 14, 28, 29, 30, 31, 32, 33, or 34, wherein said RPP is labeled.

4. (Original) A method according to claim 3, wherein said label is a fluorescent label.

5. (Original) A method according to claim 3, wherein said label is a radioisotope.

6-12. (Canceled)

13. (Currently amended) ~~A method according to claim 1~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said RPP has a sequence selected from the group consisting of the sequences depicted in Figure 3 (SEQ ID NOS:1-6);

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent, to thereby identify a candidate agent that alters the amount of said first germline mRNA.

14. (Currently amended) ~~A method according to claim 1~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said RPP has a sequence selected from the group consisting of the sequences depicted in Figure 4 (SEQ ID NOS:7-13);

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA.

15. (Canceled)

16. (Canceled)

17. (Currently amended) A method according to any one of claims [[1]] 13, 14, 28, 29, 30, 31, 32, 33, or 34, further comprising:

a) adding to said mixture at least a second RNAse protection probe (RPP) substantially complementary to a second germline mRNA to form a second hybridization complex between said second germline mRNA and said second RPP; and

b) quantifying the amount of said second germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA but not said second germline mRNA.

18. (Currently Amended) A method according to any one of claims [[1]] 13, 14, 28, 29, 30, 31, 32, 33, or 34, wherein said candidate agent is a small molecule.

19. (Currently Amended) A method according to any one of claims [[1]] 13, 14, 28, 29, 30, 31, 32, 33, or 34, wherein said candidate agent is a peptide.

20. (Previously presented) A method according to claim 19, wherein said peptide is a random peptide.

21. (Previously presented) A method according to claim 19, wherein said peptide is a partially random peptides.

22. (Previously presented) A method according to claim 19, wherein said adding is done using a retrovirus encoding said peptide.

23. (Previously presented) A method according to claim 19 wherein said adding is done using a retrovirus comprising sequence derived from a cDNA library.

24-26. (Canceled)

27. (Currently amended) The method of any one of claims [[1]] 13, 14, 28, 29, 30, 31, 32, 33, or 34, wherein said first RNAse protection probe (RPP) and said first germline mRNA contain less than 5 base mismatches.

28. (Currently amended) ~~A method according to claim 6~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said germline mRNA is Ig alpha-1, and wherein said RPP comprises the sequence set forth as SEQ ID NO:7;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA.

29. (Currently amended) ~~A method according to claim 7~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said germline mRNA is Ig alpha-2, and wherein said RPP comprises the sequence set forth as SEQ ID NO:1 or SEQ ID NO: 8;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA.

30. (Currently amended) ~~A method according to claim 8~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP)

substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said germline mRNA is Ig epsilon, and wherein said RPP comprises the sequence set forth as SEQ ID NO:2 or SEQ ID NO: 9;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA.

31. (Currently amended) ~~A method according to claim 9~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said germline mRNA is Ig gamma-1, and wherein said RPP comprises the sequence set forth as SEQ ID NO:3 or SEQ ID NO: 10;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA.

32. (Currently amended) ~~A method according to claim 10~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said

first RPP, wherein said germline mRNA is Ig gamma-2, and wherein said RPP comprises the sequence set forth as SEQ ID NO:4 or SEQ ID NO: 11;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA..

33. (Currently amended) ~~A method according to claim 11~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said germline mRNA is Ig gamma-3, and wherein said RPP comprises the sequence set forth as SEQ ID NO:5 or SEQ ID NO: 12;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA.

34. (Currently amended) ~~A method according to claim 12~~ A method for determining whether a candidate agent is capable of modulating germline transcription, comprising:

a) adding a candidate agent to a plurality of cells

b) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP, wherein said germline mRNA is Ig gamma-4, and wherein said RPP comprises the sequence set forth as SEQ ID NO:6 or SEQ ID NO: 13;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and

e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent to thereby identify a candidate agent that alters the amount of said first germline mRNA.